

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lau, Lester F.
- (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Clough, David W.
 - (B) REGISTRATION NUMBER: 36,107
 - (C) REFERENCE/DOCKET NUMBER: 28758/33766
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312/474-6300
 - (B) TELEFAX: 312/474-0448
 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 180..1316
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGAGCGCC CCAGAGAAGC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG	60
AAGGACACCC GCCGCCTCGG CCCTCGCCTC ACCGCACTCC GGGCGCATTT GATCCCGCTG	120
CTCGCCGGCT TGTTGGTTCT GTGTCGCCGC GCTCGCCCCG GTTCCTCCTG CGCGCCACA	179
ATG AGC TCC AGC ACC TTC AGG ACG CTC GCT GTC GCC GTC ACC CTT CTC	227
Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu	
1 5 10 15	
CAC TTG ACC AGA CTG GCG CTC TCC ACC TGC CCC GCC GCC TGC CAC TGC	275
His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys	
20 25 30	
CCT CTG GAG GCA CCC AAG TGC GCC CCG GGA GTC GGG TTG GTC CGG GAC	323
Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp	
35 40 45	
GGC TGC GGC TGC TGT AAG GTC TGC GCT AAA CAA CTC AAC GAG GAC TGC	371
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys	
50 55 60	
AGC AAA ACT CAG CCC TGC GAC CAC ACC AAG GGG TTG GAA TGC AAT TTC	419
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe	
65 70 75 80	
GGC GCC AGC TCC ACC GCT CTG AAA GGG ATC TGC AGA GCT CAG TCA GAA	467
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu	
85 90 95	
GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGC	515
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser	
100 105 110	
TTC CAG CCC AAC TGT AAA CAC CAG TGC ACA TGT ATT GAT GGC GCC GTG	563
Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val	
115 120 125	
GGC TGC ATT CCT CTG TGT CCC CAA GAA CTG TCT CTC CCC AAT CTG GGC	611
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly	
130 135 140	
TGT CCC AAC CCC CGG CTG GTG AAA GTC AGC GGG CAG TGC TGT GAA GAG	659
Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu	
145 150 155 160	
TGG GTT TGT GAT GAA GAC AGC ATT AAG GAC TCC CTG GAC GAC CAG GAT	707
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp	
165 170 175	
GAC CTC CTC GGA CTC GAT GCC TCG GAG GTG GAG TTA ACG AGA AAC AAT	755
Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn	
180 185 190	

GAG TTA ATC GCA ATT GGA AAA GGC AGC TCA CTG AAG AGG CTT CCT GTC	803
Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val	
195 200 205	
TTT GGC ACC GAA CCG CGA GTT CTT TTC AAC CCT CTG CAC GCC CAT GGC	851
Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly	
210 215 220	
CAG AAA TGC ATC GTT CAG ACC ACG TCT TGG TCC CAG TGC TCC AAG AGC	899
Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser	
225 230 235 240	
TGC GGA ACT GGC ATC TCC ACA CGA GTT ACC AAT GAC AAC CCA GAG TGC	947
Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys	
245 250 255	
CGC CTG GTG AAA GAG ACC CGG ATC TGT GAA GTG CGT CCT TGT GGA CAA	995
Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln	
260 265 270	
CCA GTG TAC AGC AGC CTA AAA AAG GGC AAG AAA TGC AGC AAG ACC AAG	1043
Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys	
275 280 285	
AAA TCC CCA GAA CCA GTC AGA TTT ACT TAT GCA GGA TGC TCC AGT GTC	1091
Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val	
290 295 300	
AAG AAA TAC CGG CCC AAA TAC TGC GGC TCC TGC GTA GAT GGC CGG TGC	1139
Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys	
305 310 315 320	
TGC ACA CCT CTG CAG ACC AGA ACT GTG AAG ATG CGG TTC CGA TGC GAA	1187
Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu	
325 330 335	
GAT GGA GAG ATG TTT TCC AAG AAT GTC ATG ATG ATC CAG TCC TGC AAA	1235
Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys	
340 345 350	
TGT AAC TAC AAC TGC CCG CAT CCC AAC GAG GCA TCG TTC CGA CTG TAC	1283
Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr	
355 360 365	
AGC CTA TTC AAT GAC ATC CAC AAG TTC AGG GAC TAAGTGCCTC CAGGGTTCCT	1336
Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp	
370 375	
AGTGTGGGCT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGGTGG GCGGAGGATG	1396
AATGGTGCCT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAAAGTACC AAGGGGCTGA	1456
TGTGGACGGA CAGCAGCGCA GCCG	1480

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Ser	Thr	Phe	Arg	Thr	Leu	Ala	Val	Ala	Val	Thr	Leu	Leu
1				5				10						15	
His	Leu	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His	Cys
			20					25					30		
Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg	Asp
		35					40					45			
Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp	Cys
	50					55					60				
Ser	Lys	Thr	Gln	Pro	Cys	Asp	His	Thr	Lys	Gly	Leu	Glu	Cys	Asn	Phe
65					70					75					80
Gly	Ala	Ser	Ser	Thr	Ala	Leu	Lys	Gly	Ile	Cys	Arg	Ala	Gln	Ser	Glu
				85					90					95	
Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser	Arg	Ile	Tyr	Gln	Asn	Gly	Glu	Ser
		100						105					110		
Phe	Gln	Pro	Asn	Cys	Lys	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val
		115					120					125			
Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln	Glu	Leu	Ser	Leu	Pro	Asn	Leu	Gly
	130					135					140				
Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys	Val	Ser	Gly	Gln	Cys	Cys	Glu	Glu
145				150						155					160
Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile	Lys	Asp	Ser	Leu	Asp	Asp	Gln	Asp
			165						170					175	
Asp	Leu	Leu	Gly	Leu	Asp	Ala	Ser	Glu	Val	Glu	Leu	Thr	Arg	Asn	Asn
			180					185					190		
Glu	Leu	Ile	Ala	Ile	Gly	Lys	Gly	Ser	Ser	Leu	Lys	Arg	Leu	Pro	Val
		195					200					205			
Phe	Gly	Thr	Glu	Pro	Arg	Val	Leu	Phe	Asn	Pro	Leu	His	Ala	His	Gly
	210					215					220				
Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	Ser	Lys	Ser
225					230					235					240

Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
245 250 255

Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
260 265 270

Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
275 280 285

Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
290 295 300

Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
305 310 315 320

Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
325 330 335

Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
340 345 350

Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
355 360 365

Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
370 375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1266

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCGGGCCC ACCGCGACAC CGCGCCGCCA CCCCACCCC GCTGCGCACG GCCTGTCCGC	60
TGCACACCAG CTTGTTGGCG TCTTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC	120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT	168
Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu	
1 5 10 15	
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC	216
Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His	

																20																	25																	30																
TGC	CCC	CTG	GAG	GCG	CCC	AAG	TGC	GCG	CCG	GGA	GTC	GGG	CTG	GTC	CGG																	264																																		
Cys	Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg																																																			
			35						40			45																																																						
GAC	GGC	TGC	GGC	TGC	TGT	AAG	GTC	TGC	GCC	AAG	CAG	CTC	AAC	GAG	GAC																	312																																		
Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp																																																			
			50			55			60																																																									
TGC	AGC	AAA	ACG	CAG	CCC	TGC	GAC	CAC	ACC	AAG	GGG	CTG	GAA	TGC	AAC																	360																																		
Cys	Ser	Lys	Thr	Gln	Pro	Cys	Asp	His	Thr	Lys	Gly	Leu	Glu	Cys	Asn																																																			
			65			70			75																																																									
TTC	GGC	GCC	AGC	TCC	ACC	GCT	CTG	AAG	GGG	ATC	TGC	AGA	GCT	CAG	TCA																	408																																		
Phe	Gly	Ala	Ser	Ser	Thr	Ala	Leu	Lys	Gly	Ile	Cys	Arg	Ala	Gln	Ser																																																			
80						85			90																			95																																						
GAG	GGC	AGA	CCC	TGT	GAA	TAT	AAC	TCC	AGA	ATC	TAC	CAA	AAC	GGG	GAA																	456																																		
Glu	Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser	Arg	Ile	Tyr	Gln	Asn	Gly	Glu																																																			
			100			105			110																																																									
AGT	TTC	CAG	CCC	AAC	TGT	CAA	CAT	CAG	TGC	ACA	TGT	ATT	GAT	GGC	GCC																	504																																		
Ser	Phe	Gln	Pro	Asn	Cys	Gln	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala																																																			
			115			120			125																																																									
GTG	GGC	TGC	ATT	CCT	CTG	TGT	CCC	CAA	GAA	CTA	TCT	CTC	CCC	AAC	TTG																	552																																		
Val	Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln	Glu	Leu	Ser	Leu	Pro	Asn	Leu																																																			
			130			135			140																																																									
GGC	TGT	CCC	AAC	CCT	CGG	CTG	GTC	AAA	GTT	ACC	GGG	CAG	TGC	TGC	GAG																	600																																		
Gly	Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys	Val	Thr	Gly	Gln	Cys	Cys	Glu																																																			
			145			150			155																																																									
GAG	TGG	GTC	TGT	GAC	GAG	GAT	AGT	ATC	AAG	GAC	CCC	ATG	GAG	GAC	CAG																	648																																		
Glu	Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile	Lys	Asp	Pro	Met	Glu	Asp	Gln																																																			
160			165			170			175																																																									
GAC	GGC	CTC	CTT	GGC	AAG	GAG	CTG	GGA	TTC	GAT	GCC	TCC	GAG	GTG	GAG																	696																																		
Asp	Gly	Leu	Leu	Gly	Lys	Glu	Leu	Gly	Phe	Asp	Ala	Ser	Glu	Val	Glu																																																			
			180			185			190																																																									
TTG	ACG	AGA	AAC	AAT	GAA	TTG	ATT	GCA	GTT	GGA	AAA	GGC	AGA	TCA	CTG																	744																																		
Leu	Thr	Arg	Asn	Asn	Glu	Leu	Ile	Ala	Val	Gly	Lys	Gly	Arg	Ser	Leu																																																			
			195			200			205																																																									
AAG	CGG	CTC	CCT	GTT	TTT	GGA	ATG	GAG	CCT	CGC	ATC	CTA	TAC	AAC	CCT																	792																																		
Lys	Arg	Leu	Pro	Val	Phe	Gly	Met	Glu	Pro	Arg	Ile	Leu	Tyr	Asn	Pro																																																			
			210			215			220																																																									
TTA	CAA	GGC	CAG	AAA	TGT	ATT	GTT	CAA	ACA	ACT	TCA	TGG	TCC	CAG	TGC																	840																																		
Leu	Gln	Gly	Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys																																																			
			225			230			235</																																																									

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CCT GAG TGC CGC CTT GTG AAA GAA ACC CGG ATT TGT GAG GTG CGG CCT      936
Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro
                260                      265                      270

TGT GGA CAG CCA GTG TAC AGC AGC CTG AAA AAG GGC AAG AAA TGC AGC      984
Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser
                275                      280                      285

AAG ACC AAG AAA TCC CCC GAA CCA GTC AGG TTT ACT TAC GCT GGA TGT     1032
Lys Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys
                290                      295                      300

TTG AGT GTG AAG AAA TAC CGG CCC AAG TAC TGC GGT TCC TGC GTG GAC     1080
Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp
                305                      310                      315

GGC CGA TGC TGC ACG CCC CAG CTG ACC AGG ACT GTG AAG ATG CGG TTC     1128
Gly Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe
                320                      325                      330                      335

CGC TGC GAA GAT GGG GAG ACA TTT TCC AAG AAC GTC ATG ATG ATC CAG     1176
Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln
                340                      345                      350

TCC TGC AAA TGC AAC TAC AAC TGC CCG CAT GCC AAT GAA GCA GCG TTT     1224
Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe
                355                      360                      365

CCC TTC TAC AGG CTG TTC AAT GAC ATT CAC AAA TTT AGG GAC           1266
Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
                370                      375                      380

TAAATGCTAC CTGGGTTTCC AGGGCACACC TAGACAAACA AGGGAGAAGA GTGTCAGAAT   1326

CAGAATCATG GAGAAAATGG GCGGGGGTGG TGTGGGTGAT GGGACTCATT GTAGAAAGGA   1386

AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT                                1418
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu
  1             5             10             15
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Arg	Cys	Cys	Thr	Pro	Gln	Leu	Thr	Arg	Thr	Val	Lys	Met	Arg	Phe	Arg
				325					330					335	
Cys	Glu	Asp	Gly	Glu	Thr	Phe	Ser	Lys	Asn	Val	Met	Met	Ile	Gln	Ser
			340					345					350		
Cys	Lys	Cys	Asn	Tyr	Asn	Cys	Pro	His	Ala	Asn	Glu	Ala	Ala	Phe	Pro
			355				360					365			
Phe	Tyr	Arg	Leu	Phe	Asn	Asp	Ile	His	Lys	Phe	Arg	Asp			
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Fisp12 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGCC	GACAACCCCA	GACGCCACCG	CCTGGAGCGT	CCAGACACCA	ACCTCCGCCC	60
CTGTCCGAAT	CCAGGCTCCA	GCCGCGCCTC	TCGTCGCCTC	TGCACCCTGC	TGTGCATCCT	120
CCTACCGCGT	CCCGATCATG	CTCGCCTCCG	TCGCAGGTCC	CATCAGCCTC	GCCTTGGTGC	180
TCCTCGCCCT	CTGCACCCGG	CCTGCTACGG	GCCAGGACTG	CAGCGCGCAA	TGTCAGTGCG	240
CAGCCGAAGC	AGCGCCGCAC	TGCCCCGCCG	GCGTGAGCCT	GGTGCTGGAC	GGCTGCGGCT	300
GCTGCCGCGT	CTGCGCCAAG	CAGCTGGGAG	AACTGTGTAC	GGAGCGTGAC	CCCTGCGACC	360
CACACAAGGG	CCTCTTCTGC	GATTTCGGCT	CCCCCGCCAA	CCGCAAGATT	GGAGTGTGCA	420
CTGCCAAAGA	TGGTGACACC	TGTGTCTTCG	GTGGGTCGGT	GTACCGCAGC	GGTGAGTCCT	480
TCCAAAGCAG	CTGCAAATAC	CAATGCACTT	GCCTGGATGG	GGCCGTGGGC	TGCGTGCCCC	540
TATGCAGCAT	GGACGTGCGC	CTGCCCAGCC	CTGACTGCCC	CTTCCCGAGA	AGGGTCAAGC	600
TGCCTGGGAA	ATGCTGCAAG	GAGTGGGTGT	GTGACGAGCC	CAAGGACCGC	ACAGCAGTTG	660
GCCCTGCCCT	AGCTGCCTAC	CGACTGGAAG	ACACATTTGG	CCCAGACCCA	ACTATGATGC	720
GAGCCAACTG	CCTGGTCCAG	ACCACAGAGT	GGAGCGCCTG	TTCTAAGACC	TGTGGAATGG	780
GCATCTCCAC	CCGAGTTACC	AATGACAATA	CCTTCTGCAG	ACTGGAGAAG	CAGAGCCGCC	840
TCTGCATGGT	CAGGCCCTGC	GAAGCTGACC	TGGAGGAAAA	CATTAAGAAG	GGCAAAAAGT	900

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GCATCCGGAC ACCTAAAATC GCCAAGCCTG TCAAGTTTGA GCTTTCTGGC TGCACCAAGT 960
TGAAGACATA CAGGGCTAAG TTCTGCGGGG TGTGCACAGA CGGCCGCTGC TGCACACCGC 1020
ACAGAACCAC CACTCTGCCA GTGGAGTTCA AATGCCCCGA TGGCGAGATC ATGAAAAAGA 1080
ATATGATGTT CATCAAGACC TGTGCCTGCC ATTACAACCTG TCCTGGGGAC AATGACATCT 1140
TTGAGTCCCT GTACTACAGG AAGATGTACG GAGACATGGC GTAAAGCCAG GAAGTAAGGG 1200
ACACGAACTC ATTAGACTAT AACTTGAACCT GAGTTGCATC TCATTTTCTT CTGTAAAAAC 1260
AATTACAGTA GCACATTAAT TTAAATCTGT GTTTTTAACT ACCGTGGGAG GAACTATCCC 1320
ACCAAAGTGA GAACGTTATG TCATGGCCAT ACAAGTAGTC TGTCAACCTC AGACACTGGT 1380
TTCGAGACAG TTTACACTTG ACAGTTGTTC ATTAGCGCAC AGTGCCAGAA CGCACACTGA 1440
GGTGAGTCTC CTGGAACAGT GGAGATGCCA GGAGAAAGAA AGACAGGTAC TAGCTGAGGT 1500
TATTTTAAAA GCAGCAGTGT GCCTACTTTT TGGAGTGTA CCGGGGAGGG AAATTATAGC 1560
ATGCTTGCAG ACAGACCTGC TCTAGCGAGA GCTGAGCATG TGTCTCCAC TAGATGAGGC 1620
TGAGTCCAGC TGTTCCTTAA GAACAGCAGT TTCAGCCTCT GACCATTCTG ATTCCAGTGA 1680
CACTTGTCAG GAGTCAGAGC CTTGTCTGTT AGACTGGACA GCTTGTGGCA AGTAAGTTTG 1740
CCTGTAACAA GCCAGATTTT TATTGATATT GTAAATATTG TGGATATATA TATATATATA 1800
TATATTTGTA CAGTTATCTA AGTTAATTTA AAGTCATTTG TTTTGTGTTT AAGTGCTTTT 1860
GGGATTTTAA ACTGATAGCC TCAAACCTCA AACACCATAG GTAGGACACG AAGCTTATCT 1920
GTGATTCAAA ACAAAGGAGA TACTGCAGTG GGAATTGTGA CCTGAGTGAC TCTCTGTCAG 1980
AACAAACAAA TGCTGTGCAG GTGATAAAGC TATGTATTGG AAGTCAGATT TCTAGTAGGA 2040
AATGTGGTCA AATCCCTGTT GGTGAACAAA TGGCCTTTAT TAAGAAATGG CTGGCTCAGG 2100
GTAAGGTCCG ATTCCTACCA GGAAGTGCTT GCTGCTTCTT TGATTATGAC TGGTTTGGGG 2160
TGGGGGGCAG TTTATTTGTT GAGAGTGTGA CCAAAGTTA CATGTTTGCA CCTTTCTAGT 2220
TGAAAATAAA GTATATATAT ATTTTTTATA TGAAAAAAA GGAATTC 2267

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

[illegible]

(D) OTHER INFORMATION: "Fisp12 amino acid sequence"

Met 1	Leu	Ala	Ser 5	Val	Ala	Gly	Pro	Ile	Ser 10	Leu	Ala	Leu	Val	Leu 15	Leu
Ala	Leu	Cys	Thr 20	Arg	Pro	Ala	Thr	Gly 25	Gln	Asp	Cys	Ser	Ala 30	Gln	Cys
Gln	Cys	Ala 35	Ala	Glu	Ala	Ala	Pro 40	His	Cys	Pro	Ala	Gly 45	Val	Ser	Leu
Val 50	Leu	Asp	Gly	Cys	Gly	Cys 55	Cys	Arg	Val	Cys	Ala 60	Lys	Gln	Leu	Gly
Glu 65	Leu	Cys	Thr	Glu	Arg 70	Asp	Pro	Cys	Asp 75	Pro	His	Lys	Gly	Leu	Phe 80
Cys	Asp	Phe	Gly 85	Ser	Pro	Ala	Asn	Arg	Lys 90	Ile	Gly	Val	Cys	Thr 95	Ala
Lys	Asp	Gly	Ala 100	Pro	Cys	Val	Phe	Gly 105	Gly	Ser	Val	Tyr	Arg 110	Ser	Gly
Glu	Ser	Phe 115	Gln	Ser	Ser	Cys	Lys 120	Tyr	Gln	Cys	Thr	Cys 125	Leu	Asp	Gly
Ala 130	Val	Gly	Cys	Val	Pro	Leu 135	Cys	Ser	Met	Asp	Val 140	Arg	Leu	Pro	Ser
Pro 145	Asp	Cys	Pro	Phe	Pro 150	Arg	Arg	Val	Lys	Leu 155	Pro	Gly	Lys	Cys	Cys 160
Lys	Glu	Trp	Val 165	Cys	Asp	Glu	Pro	Lys	Asp 170	Arg	Thr	Ala	Val	Gly 175	Pro
Ala	Leu	Ala 180	Ala	Tyr	Arg	Leu	Glu	Asp 185	Thr	Phe	Gly	Pro	Asp 190	Pro	Thr
Met	Met	Arg 195	Ala	Asn	Cys	Leu	Val 200	Gln	Thr	Thr	Glu	Trp 205	Ser	Ala	Cys
Ser 210	Lys	Thr	Cys	Gly	Met	Gly 215	Ile	Ser	Thr	Arg	Val 220	Thr	Asn	Asp	Asn
Thr 225	Phe	Cys	Arg	Leu	Glu 230	Lys	Gln	Ser	Arg	Leu 235	Cys	Met	Val	Arg	Pro 240
Cys	Glu	Ala	Asp	Leu 245	Glu	Glu	Asn	Ile	Lys 250	Lys	Gly	Lys	Lys	Cys 255	Ile
Arg	Thr	Pro	Lys 260	Ile	Ala	Lys	Pro	Val 265	Lys	Phe	Glu	Leu	Ser 270	Gly	Cys

Thr	Ser	Val	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr	Asp
		275					280					285			
Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Thr	Leu	Pro	Val	Glu	Phe
	290					295					300				
Lys	Cys	Pro	Asp	Gly	Glu	Ile	Met	Lys	Lys	Asn	Met	Met	Phe	Ile	Lys
305					310					315					320
Thr	Cys	Ala	Cys	His	Tyr	Asn	Cys	Pro	Gly	Asp	Asn	Asp	Ile	Phe	Glu
				325					330					335	
Ser	Leu	Tyr	Tyr	Arg	Lys	Met	Tyr	Gly	Asp	Met	Ala				
					340			345							

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: "CTGF cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG	60
CCAGCGCTCC AGGCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA	120
GTGCCAACCA TGACCGCCGC CAGTATGGGC CCCGTCCGCG TCGCCTTCGT GGTCTCCTC	180
GCCCTCTGCA GCCGGCCGGC CGTCGGCCAG AACTGCAGCG GGCCGTGCCG GTGCCCCGAC	240
GAGCCGGCGC CGCGCTGCCC GGCGGGCGTG AGCCTCGTGC TGGACGGCTG CGGCTGCTGC	300
CGCGTCTGCG CCAAGCAGCT GGGCGAGCTG TGCACCGAGC GCGACCCCTG CGACCCGCAC	360
AAGGGCCTCT TCTGTGACTT CGGCTCCCCG GCCAACCGCA AGATCGGCGT GTGCACCGCC	420
AAAGATGGTG CTCCCTGCAT CTTCGGTGGT ACGGTGTACC GCAGCGGAGA GTCCTTCCAG	480
AGCAGCTGCA AGTACCACTG CACGTGCCTG GACGGGGCGG TGGGCTGCAT GCCCCTGTGC	540
AGCATGGACG TTCGTCTGCC CAGCCCTGAC TGCCCTTCC CGAGGAGGGT CAAGCTGCCC	600
GGGAAATGCT GCGAGGAGTG GGTGTGTGAC GAGCCCAAGG ACCAAACCGT GGTGGGCCT	660
GCCCTCGCGG CTTACCGACT GGAAGACACG TTTGGCCCAG ACCCAACTAT GATTAGAGCC	720
AACTGCCTGG TCCAGACCAC AGAGTGGAGC GCCTGTTCCA AGACCTGTGG GATGGGCATC	780

TCCACCCGGG TTACCAATGA CAACGCCTCC TGCAGGCTAG AGAAGCAGAG CCGCCTGTGC	840
ATGGTCAGGC CTTGCGAAGC TGACCTGGAA GAGAACATTA AGAAGGGCAA AAAGTGCATC	900
CGTACTCCCA AAATCTCCAA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG	960
ACATACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA	1020
ACCACCACCC TGCCGGTGGA GTTCAAGTGC CCTGACGGCG AGGTCATGAA GAAGAACATG	1080
ATGTTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTTGAA	1140
TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT	1200
AACTCATTAG ACTGGAAGTT GAACTGATTC ACATCTCATT TTTCCGTAAA AATGATTTCA	1260
GTAGCACAAG TTATTTAAAT CTGTTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA	1320
AAACATTGTG CCATGTCAAA CAAATAGTCT ATCTTCCCCA GACACTGGTT TGAAGAATGT	1380
TAAGACTTGA CAGTGGAAGT ACATTAGTAC ACAGCACCAG AATGTATATT AAGGTGTGGC	1440
TTTAGGAGCA GTGGGAGGGT ACCGGCCCCG TTAGTATCAT CAGATCGACT CTTATACGAG	1500
TAATATGCCT GCTATTTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT	1560
GCCTGTAGCC CCAGTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTCAA	1620
GTGTTTCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTCGA ATGACACTGT	1680
TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTTGCCTGTA	1740
ACAAGCCAGA TTTTTTAAAA TTTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA	1800
TATATATATA TATGTACAGT TATCTAAGTT AATTTAAAGT TGTTTGTGCC TTTTTATTTT	1860
TGTTTTTAAT GCTTTGATAT TTCAATGTTA GCCTCAATTT CTGAACACCA TAGGTAGAAT	1920
GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG	1980
ATAGAATGAC AGTCCGTCAA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTTGCA	2040
GGCTGATTTT TAGGTAGGAA ATGTGGTAGC TCACG	2075

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "CTGF amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
1 5 10 15
Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
20 25 30
Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
35 40 45
Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
50 55 60
Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
65 70 75 80
Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
85 90 95
Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
100 105 110
Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
115 120 125
Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
130 135 140
Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
145 150 155 160
Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
165 170 175
Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
180 185 190
Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
195 200 205
Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
210 215 220
Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
225 230 235 240
Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
245 250 255
Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
260 265 270
Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
275 280 285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGATCCTG TGATGAAGAC AGCATT

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAATTCAA CGATGCATTT CTGGCC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp
1				5				10						15	

Cys	Ser	Lys	Thr	Gln
			20	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys
1 5 10 15

Ile Pro Leu Cys Pro
 20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly
1 5 10 15

Thr Gly Ile Ser Thr Arg Val Thr
 20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys
1 5 10 15

Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys	Cys	Thr	Pro	Leu	Gln
1				5				10						15	

Thr	Arg	Thr	Val	Lys
			20	

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